

1/2/02  
A-378CIP5.ST25.txt  
SEQUENCE LISTING

<110> BOYLE, WILLIAM J.  
LACEY, DAVID LEE  
CALZONE, FRANK J.  
CHANG, MING-SHI  
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

<130> A-378CIP5

<140> US 09/613,591

<141> 2000-07-10

<150> US 09/457,647

<151> 1999-12-09

<150> US 09/350,670

<151> 1999-07-09

<150> US 08/706,945

<151> 1996-09-03

<150> US 08/577,788

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<210> 108  
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<223> PCR primer for FchOPG fusion protein.

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<223> Fc/muOPG

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<220>
<221> misc_feature
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tt

62

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Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp  
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Asp Trp His  
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 Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile  
 1 5 10 15

att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat 216  
 Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr  
 20 25 30

gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc 264  
 Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly  
 35 40 45

acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc 312  
 Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val  
 50 55 60

cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa 360  
 Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu  
 65 70 75

tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag 408  
 Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln  
 80 85 90 95

gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc 456  
 Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg

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Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Gly	Glu	Thr	Ser	Ser	Lys	Ala	Pro			
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Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Ser	Leu	Gly	Leu	Leu	Leu	Ile	Gln			
160					165					170					175			
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Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Val	Cys	Ser	Gly	Asn	Arg	Glu	Ala			
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Thr	Gln	Asn	Cys	Glu	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe			
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Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	Pro	Asn	Trp	Leu	Ser	Val	Leu			
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Val	Asp	Ser	Leu	Pro	Gly	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg				
	225				230					235								
ata	aaa	cgg	aga	cac	agc	tcg	caa	gag	caa	act	ttc	cag	cta	ctt	aag	888		
Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys			
240					245					250					255			
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Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	Glu	Met	Val	Lys	Lys	Ile	Ile			
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caa	gac	att	gac	ctc	tgt	gaa	agc	agt	gtg	caa	cgg	cat	atc	ggc	cac	984		
Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	Val	Gln	Arg	His	Ile	Gly	His			
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Lys	Pro	Ser	Glu	Gln	Leu	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys			
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Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	Tyr	Ala	Leu	Lys	His			
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ttg	aaa	gca	tac	cac	ttt	ccc	aaa	acc	gtc	acc	cac	agt	ctg	agg	aag	1224		
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370

375

380

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Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser
385 390 395

tgc tta tagttaggaa tggctactgg gctgtttctt caggatgggc caacactgat 1376
Cys Leu
400

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<210> 121
<211> 401
<212> PRT
<213> Rattus rattus

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<400> 121

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Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
20 25 30

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Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

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Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

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Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
180 185 190

Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala  
275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly  
290 295 300

Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
305 310 315 320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
325 330 335

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Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
 340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
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Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
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Leu

<210> 122  
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 Met Asn Lys Trp Leu Cys Cys Ala  
 1 5

ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 162  
 Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu  
 10 15 20

ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 210  
 Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu  
 25 30 35 40

tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 258  
 Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val  
 45 50 55

agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 306  
 Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp  
 60 65 70

agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 354  
 Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys  
 75 80 85

gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 402  
 Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val

## A-378CIP5.ST25.txt

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tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys 105 110 115 120			450
cac cgg agc tgt ccc ccg ggc tcc ggc gtg gtg caa gct gga acc cca His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala Gly Thr Pro 125 130 135			498
gag cga aac aca gtt tgc aaa aaa tgt cca gat ggg ttc ttc tca ggt Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe Phe Ser Gly 140 145 150			546
gag act tca tcg aaa gca ccc tgt ata aaa cac acg aac tgc agc aca Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn Cys Ser Thr 155 160 165			594
ttt ggc ctc ctg cta att cag aaa gga aat gca aca cat gac aac tgt Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His Asp Asn Cys 170 175 180			642
tgt tcc gga aac aga gaa gcc acg caa aag tgt gga ata gat gtc acc Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile Asp Val Thr 185 190 195 200			690
ctg tgt gaa gag gcc ttc ttc agg ttt gct gtt cct acc aag att ata Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Ile Ile 205 210 215			738
cca aat tgg ctg agt gtt ttg gtg gac agt ttg cct ggg acc aaa gtg Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly Thr Lys Val 220 225 230			786
aat gcc gag agt gta gag agg ata aaa cgg aga cac agc tca caa gag Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser Gln Glu 235 240 245			834
caa acc ttc cag ctg ctg aag ctg tgg aaa cat caa aac aga gac cag Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Arg Asp Gln 250 255 260			882
gaa atg gtg aag aag atc atc caa gac att gac ctc tgt gaa agc agc Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Ser Ser 265 270 275 280			930
gtg cag cgg cat ctc ggc cac tcg aac ctc acc aca gag cag ctt ctt Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu Gln Leu Leu 285 290 295			978
gcc ttg atg gag agc ctg cct ggg aag aag atc agc cca gaa gag att Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro Glu Glu Ile 300 305 310			1026
gag aga acg aga aag acc tgc aaa tcg agc gag cag ctc ctg aag cta Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu Leu Lys Leu 315 320 325			1074
ctc agt tta tgg agg atc aaa aat ggt gac caa gac acc ttg aag ggc Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly 330 335 340			1122
ctg atg tat gcc ctc aag cac ttg aaa aca tcc cac ttt ccc aaa act Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe Pro Lys Thr 345 350 355 360			1170
gtc acc cac agt ctg agg aag acc atg agg ttc ctg cac agc ttc aca Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His Ser Phe Thr			1218

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```

365                                370                                375
atg tac aga ctg tat cag aag ctc ttt tta gaa atg ata ggg aat cag      1266
Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln
380                                385                                390

gtt caa tcc gtg aaa ata agc tgc tta taactaggaa tggtcactgg      1313
Val Gln Ser Val Lys Ile Ser Cys Leu
395                                400

gctgtttctt ca      1325

<210> 123
<211> 401
<212> PRT
<213> Mus musculus

<220>
<221> misc_feature
<222> (11)..(11)
<223> At position 11, R is a purine.

<400> 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp
20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro
50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys
145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys
165 170 175

```

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Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr  
180 185 190  
.  
Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205  
Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
210 215 220  
Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
225 230 235 240  
Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255  
Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
260 265 270  
Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser  
275 280 285  
Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly  
290 295 300  
Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
305 310 315 320  
Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
325 330 335  
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
340 345 350  
Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
355 360 365  
Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
370 375 380  
Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
385 390 395 400

Leu

<210> 124  
<211> 1356  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

```
<222>    (95) .. (1297)
<223>
```

```
<220>
<221> misc_feature
<222> (63)..(63)
<223> At position 63, Y is a pyrimidine.
```

<400> 124																
gtatatataa		cgtgatgagc		gtacgggtgc		ggagacgcac		cggcgcgctc		gccagccgc						60
cgycaccaag		cccctgaggt		ttccggggac		caca		atg	aac	aag	ttg	ctg	tgc	tgc		115
								Met	Asn	Lys	Leu	Leu	Cys	Cys		
								1				5				
gcg	ctc	gtg	ttt	ctg	gac	atc	tcc	att	aag	tgg	acc	acc	cag	gaa	acg	163
Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	
		10				15						20				
ttt	cct	cca	aag	tac	ctt	cat	tat	gac	gaa	gaa	acc	tct	cat	cag	ctg	211
Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	
		25				30				35						
ttg	tgt	gac	aaa	tgt	cct	cct	ggg	acc	tac	cta	aaa	caa	cac	tgt	aca	259
Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	
		40		45						50		55				
gca	aag	tgg	aag	tcc	gtg	tgc	gcc	cct	tgc	cct	gac	cac	tac	tac	aca	307
Ala	Lys	Trp	Lys	Ser	Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	
				60				65				70				
gac	agc	tgg	cac	acc	agt	gac	gag	tgt	cta	tac	tgc	agc	ccc	gtg	tgc	355
Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	
								80				85				
aag	gag	ctg	cag	tac	gtc	aag	cag	gag	tgc	aat	cgc	acc	cac	aac	cgc	403
Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	
		90				95						100				
gtg	tgc	gaa	tgc	aag	gaa	ggg	cgc	tac	ctt	gag	ata	gag	ttc	tgc	ttg	451
Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	
		105				110				115						
aaa	cat	agg	agc	tgc	cct	cct	gga	ttt	gga	gtg	gtg	caa	gct	gga	acc	499
Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	
		120		125						130				135		
cca	gag	cga	aat	aca	gtt	tgc	aaa	aga	tgt	cca	gat	ggg	ttc	ttc	tca	547
Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	
				140				145				150				
aat	gag	acg	tca	tct	aaa	gca	ccc	tgt	aga	aaa	cac	aca	aat	tgc	agt	595
Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	
		155						160				165				
gtc	ttt	ggg	ctc	ctg	cta	act	cag	aaa	gga	aat	gca	aca	cac	gac	aac	643
Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	
		170				175						180				
ata	tgt	tcc	gga	aac	agt	gaa	tca	act	caa	aaa	tgt	gga	ata	gat	gtt	691
Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	
		185				190				195						
acc	ctg	tgt	gag	gag	gca	ttc	ttc	agg	ttt	gct	ggt	cct	aca	aag	ttt	739
Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val					

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acg cct aac tgg ctt agt gtc ttg gta gac aat ttg cct ggc acc aaa	787
Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys	
220 225 230	
gta aac gca gag agt gta gag agg ata aaa cgg caa cac agc tca caa	835
Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln	
235 240 245	
gaa cag act ttc cag ctg ctg aag tta tgg aaa cat caa aac aaa gcc	883
Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala	
250 255 260	
caa gat ata gtc aag aag atc atc caa gat att gac ctc tgt gaa aac	931
Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn	
265 270 275	
agc gtg cag cgg cac att gga cat gct aac ctc acc ttc gag cag ctt	979
Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu	
280 285 290 295	
cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga gca gaa gac	1027
Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp	
300 305 310	
att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag atc ctg aag	1075
Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys	
315 320 325	
ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac acc ttg aag	1123
Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys	
330 335 340	
ggc cta atg cac gca cta aag cac tca aag acg tac cac ttt ccc aaa	1171
Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys	
345 350 355	
act gtc act cag agt cta aag aag acc atc agg ttc ctt cac agc ttc	1219
Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe	
360 365 370 375	
aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg ata ggt aac	1267
Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn	
380 385 390	
cag gtc caa tca gta aaa ata agc tgc tta taactggaaa tggccattga	1317
Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
395 400	
gctgtttcct cacaattggc gagatcccat ggatgataa	1356

<210> 125  
 <211> 401  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (63)..(63)  
 <223> At position 63, Y is a pyrimidine.

<400> 125

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
1				5					10					15	



## A-378CIP5.ST25.txt

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro  
 50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln  
 260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 275 280 285

## A-378CIP5.ST25.txt

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400

Leu

<210> 126  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens  
 <400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys  
 1 5 10 15

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
 20 25 30

Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala  
 35 40 45

Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys  
 50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr  
 65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn  
 85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His  
 100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly  
 Page 34

115

120

125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys  
 130 135

<210> 127  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> huOPG

<400> 127  
 acctacttct ttgaagagta gtcgacgaca cactatttac aggcggcc

48

<210> 128  
 <211> 219  
 <212> PRT  
 <213> Rattus rattus

<400> 128

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
 1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
 20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
 35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
 100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
 115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
 130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr  
 145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp  
 165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg  
 180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly  
 195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr  
 210 215

<210> 129  
 <211> 281  
 <212> PRT  
 <213> Rattus rattus

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Thr Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr  
 65 70 75 80

Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His  
 85 90 95

Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln  
 100 105 110

Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys  
 115 120 125

Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys  
 130 135 140

Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln  
 145 150 155 160

Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg  
 165 170 175

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys  
 180 185 190

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```

Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp
    195                                200                205

Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys
    210                                215                220

Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp
    225                                230                235                240

Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
    245                                250                255

Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro
    260                                265                270

Ser Phe Ser Pro Thr Pro Gly Phe Thr
    275                                280

<210> 130
<211> 207
<212> PRT
<213> Rattus rattus

<400> 130

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly
 1      5      10      15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp
    20      25      30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr
    35      40      45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys
    50      55      60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val
    65      70      75      80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys
    85      90      95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys
    100     105     110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys
    115     120     125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr
    130     135     140

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Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro  
145 150 155 160

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn  
165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn  
180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr  
195 200 205

<210> 131  
<211> 227  
<212> PRT  
<213> Rattus rattus  
  
<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln  
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
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180

185

190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
210 215 220

Gln His Thr  
225

<210> 132  
<211> 197  
<212> PRT  
<213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr  
1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu  
20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr  
35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser  
50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His  
65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr  
85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr  
100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly  
115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His  
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys  
145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln  
165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met  
180 185 190

Arg Ala Leu Leu Val  
195

<210> 133  
<211> 208  
<212> PRT  
<213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

<210> 134  
<211> 224  
<212> PRT



&lt;213&gt; Rattus rattus

&lt;400&gt; 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu  
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Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys  
20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn  
35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys  
50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr  
65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser  
85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly  
100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys  
115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr  
130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His  
145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln  
165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro  
180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr  
195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile  
210 215 220

&lt;210&gt; 135

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Rattus rattus

&lt;400&gt; 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu  
Page 41

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1              5              10              15
Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro
      20              25              30
Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val
      35              40              45
Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro
      50              55              60
Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr
      65              70              75
Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro
      85              90              95
Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln
      100              105              110
Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly
      115              120              125
His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys
      130              135              140
Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp
      145              150              155
Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr
      165              170              175
Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp
      180              185              190
Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val
      195              200              205

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<212> PRT
<213> Rattus rattus

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<400> 136

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      20              25              30
Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro
      35              40              45

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Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys  
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr  
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro  
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr  
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn  
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg  
130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro  
145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu  
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu  
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54

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<400> 138

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala  
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Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe  
20 25 30

Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn  
35 40 45

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Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His  
50 55 60

Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile  
65 70 75 80

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
85 90 95

Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly  
100 105 110

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser  
115 120 125

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
130 135 140

Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Ala Leu Cys  
145 150 155 160

Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu  
165 170 175

Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro  
180 185 190

Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu  
195 200 205

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
210 215 220

Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe  
225 230 235 240

Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His  
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Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
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Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
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<210> 139  
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 35 40 45  
 Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro  
 50 55 60  
 Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His  
 65 70 75 80  
 Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
 85 90 95  
 Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala  
 100 105 110  
 Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe  
 115 120 125  
 Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
 130 135 140  
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His  
 145 150 155 160  
 Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile  
 165 170 175  
 Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
 180 185 190  
 Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly  
 195 200 205  
 Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser  
 210 215 220  
 Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
 225 230 235 240  
 Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
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 Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu  
 260 265 270

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Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala  
275 280 285

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile  
290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe  
325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His  
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Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
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